

**Version of Amended Claims With Markings to Show Changes Made:**

4. (Twice Amended) An isolated nucleic acid molecule consisting of a nucleotide sequence selected from the group consisting of:
- (a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
  - (b) a nucleotide sequence consisting of SEQ ID NO:1; [and]
  - (c) a nucleotide sequence consisting of SEQ ID NO:3; and
  - (d) [(c)] a nucleotide sequence that is completely complementary over the entire length of [to] a nucleotide sequence of (a)-(c) [(b)].
8. (Twice Amended) A [nucleic acid] vector comprising the nucleic acid molecule of claim 4.
24. (Amended) A process for producing a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the process comprising culturing the host cell of claim 9 under conditions sufficient for the production of said polypeptide, and recovering said polypeptide, thereby producing said polypeptide.

**Version of Amended Specification Paragraphs With Markings to Show Changes  
Made:**

*NOTE: Deletions are marked by brackets and bold text.*

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package [(available at <http://www.gcg.com>)], using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)) [(available at <http://www.gcg.com>)], using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (*CABIOS*, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, word length = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, word length = 3, to obtain amino acid sequences homologous to the proteins of the invention. To obtain

gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. [See <http://www.ncbi.nlm.nih.gov>.]

## REMARKS

Applicants have studied the Office Action mailed January 13, 2003 and have made amendments to the claims. It is respectfully submitted that the application, as amended, is in condition for allowance. Reconsideration and allowance of the pending claims in view of the above amendments and following remarks is respectfully requested.

### **Election/restrictions:**

Applicants acknowledge the reconsideration of the restriction requirement set forth in the Office Action mailed August 7, 2002 and, in particular, the consequent rejoinder of groups III and IV.

In view of that, Applicants are hereby re-claiming the nucleic acid sequence of SEQ ID NO:3. Specifically, Applicants are amending claim 4(c) and presenting new claim 29 directed to SEQ ID NO:3, as indicated above.

### **Sequence listing requirements & formal drawings:**

The Examiner stated that the communication filed July 17, 2002, is not fully responsive to the Office communication mailed June 19, 2002, and thus the Application does not comply with the requirements of the sequence rules.

Applicants have noticed formatting errors in the Substitute Sequence Listing filed July 17, 2002, and are therefore hereby submitting a Second Substitute Sequence Listing to correct the formatting errors (no changes have been made to the content of the Second Substitute Sequence Listing compared with the Substitute Sequence Listing, except that an amino acid sequence disclosed in the alignment on page 2 of Figure 2 has been inserted as SEQ ID NO:5, and references to "Homo sapien" in the organism field have been changed to "Homo sapiens"). Please replace the Substitute Sequence Listing filed July 17, 2002, with the Second Substitute Sequence Listing submitted herewith.

Furthermore, Applicants are also hereby submitting formal drawings in which each sequence is identified by a sequence identification number.

Applicants believe that the application now fully complies with the sequence rules.

**Hyperlinks in specification:**

The Examiner objected to the disclosure for containing hyperlinks and/or other forms of browser-executable code.

In response, Applicants have hereby deleted all hyperlinks from the specification, as indicated above by the amended specification paragraphs. The hyperlinks are not needed for enablement of the claimed invention, but merely provided additional background information.

**Rejection of claims 24 and 26 under 35 USC §112, 2<sup>nd</sup> paragraph:**

The Examiner rejected claims 24 and 26 under 35 USC §112, 2<sup>nd</sup> paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. In making the rejections, the Examiner stated that claim 24 is vague and indefinite because it cannot be ascertained which polypeptide expressed by the host cell of claim 9 is to be produced by the claimed, and, moreover, the claim does not recite a positive correlation step that relates back to the preamble of the claim. With respect to claim 26, the Examiner stated that the claim is indefinite because the vector of claim 8, from which claim 26 depends, is a nucleic acid vector; however, the Examiner does not consider a virus nor a bacteriophage, as recited in claim 26, to be a nucleic acid vector. The Examiner suggested amendments to obviate each of these grounds of rejection.

Applicants have amended claims 8 and 24, as indicated above, to clarify the metes and bounds of the claimed subject matter.

**Rejection of claim 4 under 35 USC §102(b):**

The Examiner rejected claim 4 under 35 USC §102(b) as being anticipated by Boehringer Mannheim Biochemicals, 1994 catalog (No. 1034 731/1006 924), page 93.

Applicants have amended claim 4(d), as indicated above, to clarify that the nucleotide sequence of claim 4(d) is complementary over the entire length of a nucleotide sequence recited in parts (a)-(c) of claim 4. This obviates the rejection of claim 4 under 35 USC §102(b) as being anticipated by Boehringer Mannheim because, for one thing, Boehringer Mannheim only teaches random primers that are 6 nucleotides in length, and such primers would clearly not be complementary over the entire length of a nucleotide sequence recited in parts (a)-(c) of claim 4.

### Conclusions

By way of the above amendments, claims 4, 8, and 24 have been amended and claim 29 has been added. As such, claims 4, 8-9, and 24-29 are presently pending.

Claims 8, 9, 25, 27, and 28 are allowable, as indicated in the Office Action mailed January 13, 2003.

The amendments to the specification and claims, including the newly added claim, add no new subject matter and their entry is respectfully requested.

In view of the above amendments and remarks, Applicants respectfully submit that the application and claims are in condition for allowance, and request that the Examiner reconsider and withdraw the objections and rejections. If for any reason the Examiner finds the application other than in condition for allowance, the Examiner is invited to call the undersigned agent at (240) 453-3812 should the Examiner believe a telephone interview would advance prosecution of the application.

Respectfully submitted,

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